



Blast 2 Sequences results

PubMed

Entrez

BLAST

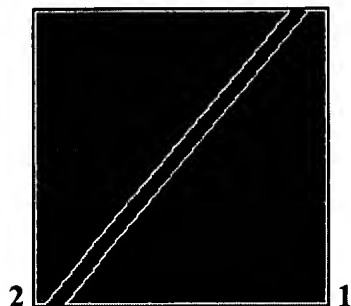
OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2030), Expect = 0.0

Identities = 377/530 (71%), Positives = 435/530 (81%), Gaps = 3/530 (0%)

```
Query: 42  MRSDKSALVFLLLQLFCVGCFCGKVLVWPCDSHWNLVKVI LLEELIVRGHEVTVLTHSK 101
          M   K A   LLL L C G GFCGKVLVWPC+MSHWN+K +LEEL+ RGHEVTVL T S
Sbjct: 1   MAPGKLASAVLLLLCCAGSGFCGKVLVWPCMSHWN LKTLLEELV KRGHEVTVL T LSN 60

Query: 102 PSLIDYRKPSALKFEVVHMPQDRTEENEI ---FVDLALNVLPGLSTWQSVIKLNDFFVEI 158
          IDY + A FEV+ +P D+   I  F++LA+NV+P + WQS  L FFV+I
Sbjct: 61  NLFIDYNRHPAFNFEVIPVPTDKNMSENILNEFIELAVNVMP TMLWQSGKLLQQFFVQI 120

Query: 159 RGT LKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVPFVLT LRISVGGN 218
          L + C + +YNQ+LMKKL+++ YDV++ DPVIPCG+L+AE+L VPFV  L+ S+G
Sbjct: 121 TEDLGLNCRNTVYNQSLMKKL RDSKYDVLVTD PVIPCGELVAEMLGVPFVNMLKFSMGHT 180

Query: 219 MERSCGKL PAPLSYVPVPM TGLTDRMTFLERVKNSMLS VLFHFWIQDYDYHFWEEFY SKA 278
          +E+ CG+LPAP SYVPV+ GLT RMTF+ERVKN + SVLF FWIQ YDY FW++FYS+A
Sbjct: 181 IEKYCGQLPAPPSYVPVPLGGLTTRMTFMERVKNMVFSVLFDFW IQQYDYKFWDQFYSEA 240

Query: 279 LGRPTTL CETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSS 338
          LGRPTTLCE +GKAEIWLIRTYWDFEFP+PY PNFEFVGGLHCKPAK LPKEME FVQSS
Sbjct: 241 LGRPTTLCEIMGKAEIWLIRTYWDFEFP RPYLPNFEFVGGLHCKPAKPLPKEME EFVQSS 300

Query: 339 GEDGIVVFSLSGLFQNVTEEKAN IASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQ 398
          GEDG+VVFSLGS+ +N+TEEKAN+IASALAQIPQKVLWRYKGKKP+TLG NTRL+DWIPQ
Sbjct: 301 GEDGVVVFSLGSMVKNLTEEKANLIASALAQIPQKVLWRYKGKKPATLGP NTRLFDWIPQ 360

Query: 399 NDLLGHPKTKAFITHGGMNGIYEAIYHGVP MVGVP IFGDQLDNIAHMKAKGA AVEINFKT 458
          NDLLGHPKTKAFITHGG NGIYEAIYHGVP MVG+PIF DQ DN+A MKAKGA AVE+N T
Sbjct: 361 NDLLGHPKTKAFITHGGSNGIYEAIYHGVP MVGMPIFSDQPDNLAGMKAKGA AVEVNMNT 420

Query: 459 MTSEDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA 518
          MTS DLL ALRTVI D +YKENAM+LSRIHHDQPVKPLDRA FW+EFVM HKGAKHLR A
```

Sbjct: 421 MTSADLLGALRTVINDPTYKENAMKLSRIHHDQPVKPLDRAAFWVEFVMHHKGAKHLRVA 480

Query: 519 AHDLTWFQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE 568
AHDL+WFQ++S+DVIGFLL CVA+AI L TKC LFS Q F K K K+E

Sbjct: 481 AHDLSWFQYHSLDVIGFLLACVASAILLVTKCCLFSFQNFQIKIGKRIKKE 530

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
0.325	0.139	0.434

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2771

Number of Sequences: 0

Number of extensions: 231

Number of successful extensions: 2

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 631

length of database: 608,447,635

effective HSP length: 135

effective length of query: 496

effective length of database: 608,447,500

effective search space: 301789960000

effective search space used: 301789960000

T: 9

A: 40

X1: 15 (7.0 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 79 (35.0 bits)